

**RAW SEQUENCE LISTING
PATENT APPLICATION US/07/800,364 B**DATE: 02/23/95
TIME: 10:51:44
*217***INPUT SET: S2404.raw**

This Raw Listing contains the General
Information Section and up to the first 5 pages.

1 **SEQUENCE LISTING**
23 (1) General Information:
45 (i) APPLICANT: Hewick, Rodney M.
6 Wang, Jack H.
7 Wozney, John M.
8 Celeste, Anthony J.9
10 (ii) TITLE OF INVENTION: Bone and Cartilage Inductive Proteins
1112 (iii) NUMBER OF SEQUENCES: 15
1314 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
16 (B) STREET: 87 CambridgePark Drive
17 (C) CITY: Cambridge
18 (D) STATE: MA
19 (E) COUNTRY: USA
20 (F) ZIP: 02140
2122 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: Floppy disk
24 (B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
2728 (vi) CURRENT APPLICATION DATA:
29 (A) APPLICATION NUMBER: US 07/800,364
30 (B) FILING DATE: 26-NOV-1991
31 (C) CLASSIFICATION:
3233 (viii) ATTORNEY/AGENT INFORMATION:
34 (A) NAME: Kapinos, Ellen J.
35 (B) REGISTRATION NUMBER: 32,245
36 (C) REFERENCE/DOCKET NUMBER: GI 5182A
3738 (ix) TELECOMMUNICATION INFORMATION:
39 (A) TELEPHONE: 617-876-1170
40 (B) TELEFAX: 617-876-5851
4142 (2) INFORMATION FOR SEQ ID NO:1:
4344 (i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 23 amino acids
46**ENTERED**

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47 (B) TYPE: amino acid
48 (C) STRANDEDNESS: single
49 (D) TOPOLOGY: unknown
50
51 (ii) MOLECULE TYPE: peptide
52
53 (iii) HYPOTHETICAL: NO
54
55 (iv) ANTI-SENSE: NO
56
57 (vi) ORIGINAL SOURCE:
58 (F) TISSUE TYPE: Bone
59
60
61 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
62
63 Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu Asp Trp
64 1 5 10 15
65
66 Val Ile Ala Pro Gln Gly Tyr
67 20
68
69 (2) INFORMATION FOR SEQ ID NO:2:
70
71 (i) SEQUENCE CHARACTERISTICS:
72 (A) LENGTH: 18 amino acids
73 (B) TYPE: amino acid
74 (C) STRANDEDNESS: single
75 (D) TOPOLOGY: unknown
76
77 (ii) MOLECULE TYPE: peptide
78
79 (iii) HYPOTHETICAL: NO
80
81 (iv) ANTI-SENSE: NO
82
83 (v) FRAGMENT TYPE: internal
84
85 (vi) ORIGINAL SOURCE:
86 (A) ORGANISM: Bos taurus
87 (F) TISSUE TYPE: Bone
88
89
90 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
91
92 Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile
93 1 5 10 15
94
95 Leu Arg
96
97
98 (2) INFORMATION FOR SEQ ID NO:3:
99

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100 (i) SEQUENCE CHARACTERISTICS:
101 (A) LENGTH: 7 amino acids
102 (B) TYPE: amino acid
103 (C) STRANDEDNESS: single
104 (D) TOPOLOGY: unknown
105
106 (ii) MOLECULE TYPE: peptide
107
108 (iii) HYPOTHETICAL: NO
109
110 (iv) ANTI-SENSE: NO
111
112 (vi) ORIGINAL SOURCE:
113 (A) ORGANISM: Bos taurus
114 (F) TISSUE TYPE: Bone
115
116
117 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
118
119 Ala Cys Cys Ala Pro Thr Lys
120 1 5
121
122 (2) INFORMATION FOR SEQ ID NO:4:
123
124 (i) SEQUENCE CHARACTERISTICS:
125 (A) LENGTH: 23 amino acids
126 (B) TYPE: amino acid
127 (C) STRANDEDNESS: single
128 (D) TOPOLOGY: unknown
129
130 (ii) MOLECULE TYPE: peptide
131
132 (iii) HYPOTHETICAL: NO
133
134 (vi) ORIGINAL SOURCE:
135 (A) ORGANISM: Bos taurus
136 (F) TISSUE TYPE: Bone
137
138
139 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
140
141 Thr Asn Glu Leu Pro Pro Pro Asn Lys Leu Pro Gly Ile Phe Asp Asp
142 1 5 10 15
143
144 Val His Gly Ser His Gly Arg
145 20
146
147 (2) INFORMATION FOR SEQ ID NO:5:
148
149 (i) SEQUENCE CHARACTERISTICS:
150 (A) LENGTH: 80 base pairs
151 (B) TYPE: nucleic acid
152 (C) STRANDEDNESS: double

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153 (D) TOPOLOGY: linear
154
155 (ii) MOLECULE TYPE: DNA (genomic)
156
157 (iii) HYPOTHETICAL: NO
158
159 (iv) ANTI-SENSE: NO
160
161 (vi) ORIGINAL SOURCE:
162 (A) ORGANISM: Bos taurus
163
164 (vii) IMMEDIATE SOURCE:
165 (B) CLONE: acc30
166
167 (viii) POSITION IN GENOME:
168 (C) UNITS: bp
169
170 (ix) FEATURE:
171 (A) NAME/KEY: CDS
172 (B) LOCATION: 25..57
173
174
175 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
176
177 GGATCCGCGT GCTGTGCTCC GACC AAG CTG AGC GCC ACC TCC GTG CTC TAC 51
178 Lys Leu Ser Ala Thr Ser Val Leu Tyr
179 1 5
180
181 TAC GAC AGCACCAACA ATGTAATTCT AGA 80
182 Tyr Asp
183 10
184
185
186 (2) INFORMATION FOR SEQ ID NO:6:
187
188 (i) SEQUENCE CHARACTERISTICS:
189 (A) LENGTH: 11 amino acids
190 (B) TYPE: amino acid
191 (D) TOPOLOGY: linear
192
193 (ii) MOLECULE TYPE: protein
194
195 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
196
197 Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp
198 1 5 10
199
200 (2) INFORMATION FOR SEQ ID NO:7:
201
202 (i) SEQUENCE CHARACTERISTICS:
203 (A) LENGTH: 199 base pairs
204 (B) TYPE: nucleic acid
205 (C) STRANDEDNESS: double

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206 (D) TOPOLOGY: linear
207
208 (ii) MOLECULE TYPE: DNA (genomic)
209
210 (iii) HYPOTHETICAL: NO
211
212 (vi) ORIGINAL SOURCE:
213 (A) ORGANISM: Bos taurus
214
215 (vii) IMMEDIATE SOURCE:
216 (A) LIBRARY: Bovine genomic
217 (B) CLONE: Lambda 9800-10
218
219 (viii) POSITION IN GENOME:
220 (C) UNITS: bp
221
222 (ix) FEATURE:
223 (A) NAME/KEY: exon
224 (B) LOCATION: 30..199
225
226 (ix) FEATURE:
227 (A) NAME/KEY: intron
228 (B) LOCATION: 1..29
229
230 (ix) FEATURE:
231 (A) NAME/KEY: CDS
232 (B) LOCATION: 30..179
233
234
235 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7: 53
236
237 TGCCCGCTGC CCCCTCCCGC CCCCCGCCAG GTG CAC CTG CTG AAG CCG CAC GCG
238 Val His Leu Leu Lys Pro His Ala
239 1 5
240
241 GTC CCC AAG GCG TGC TGC GCG CCC ACC AAG CTG AGC GCC ACT TCC GTG 101
242 Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val
243 10 15 20
244
245 CTC TAC TAC GAC AGC AGC AAC AAC GTC ATC CTG CGC AAG CAC CGC AAC 149
246 Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn
247 25 30 35 40
248
249 ATG GTG GTC CGC GCC TGC GGC TGC CAC TGAGGCCCA ACTCCACCGG 196
250 Met Val Val Arg Ala Cys Gly Cys His
251 45 50
252
253 CAG 199
254
255
256 (2) INFORMATION FOR SEQ ID NO:8:
257
258 (i) SEQUENCE CHARACTERISTICS:

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION **US/07/800,364**

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